

GenCore version 5.1.7
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OM protein - protein search, using sw model
Run on: March 31, 2006, 13:13:34 ; Search time 44 Seconds
(without alignments)
1618.191 Million cell updates/sec

Title: US-09-743-647A-35
Perfect score: 3839
Sequence: 1 MQWTKVLGLGLGAAALLGLG.....SIVVTALEGAATLRPVADL 740

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5
Searched: 283416 seqs, 96216763 residues
Total number of hits satisfying chosen parameters: 283416
Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR_80:*

1: pir1:*

2: pir2:*

3: pir3:*

4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	1307	34.0	750	2	A56881	prostate-specific
2	973.5	25.4	751	2	T30154	hypothetical prote
3	903	23.5	1483	2	T19751	hypothetical prote
4	865.5	22.5	703	2	T47631	Peptidase-like pro
5	598	15.6	757	2	A48592	transferrin recept
6	593	15.4	776	1	JH0570	transferrin recept
7	583.5	15.2	760	1	JXHU	transferrin recept
8	559.5	14.6	622	2	A34549	transferrin recept
9	557	14.5	763	1	S29548	transferrin recept
10	528.5	13.8	794	2	T40289	hypothetical prote
11	496.5	12.9	811	2	S57149	probable membrane
12	426	11.1	280	2	E85075	probable peptidase
13	305	7.9	783	2	S65188	secretory protein
14	269	7.0	809	2	S67153	probable membrane
15	211	5.5	466	2	E84132	aminopeptidase BH3
16	191	5.0	467	2	G87564	aminopeptidase, pr
17	186	4.8	529	2	G82759	hypothetical prote
18	185	4.8	455	2	S39663	aminopeptidase hom
19	176	4.6	536	2	B83278	probable aminopept
20	174	4.5	500	2	H70629	probable AMINOPEPT
21	172.5	4.5	840	2	T02164	hypothetical prote

22	172	4.5	430	2	A87634	peptidase, M20/M25
23	165	4.3	805	2	G87662	peptidase, M20/M25
24	158.5	4.1	501	2	C82414	aminopeptidase VCA
25	157.5	4.1	571	2	H87600	hypothetical prote
26	155.5	4.1	504	2	S24314	bacterial leucyl a
27	147.5	3.8	449	2	H97249	protein containing
28	146	3.8	284	2	S66427	aminopeptidase (EC
29	145	3.8	537	2	A54134	aminopeptidase Y (
30	144.5	3.8	488	2	A87569	peptidase M20/M25/
31	142.5	3.7	647	2	A83606	hypothetical prote
32	136.5	3.6	1331	2	A72647	probable surface 1
33	131	3.4	468	2	F87359	leucine aminopepti
34	129.5	3.4	493	2	T46974	leucyl aminopeptid
35	126	3.3	441	2	A84351	hypothetical prote
36	123.5	3.2	1274	2	E81779	proline dehydrogen
37	123	3.2	886	2	T35469	probable ATP /GTP-
38	122.5	3.2	2297	2	T34918	polyketide synthas
39	122	3.2	1331	2	AE1843	hypothetical prote
40	121.5	3.2	1201	2	F81202	proline dehydrogen
41	118	3.1	433	2	F84215	aminopeptidase [im
42	116.5	3.0	909	2	G69599	aconitate hydratas
43	116	3.0	567	2	C72698	hypothetical prote
44	116	3.0	2175	1	GNNYBE	genome polyprotein
45	116	3.0	4735	2	T17463	rifamycin polyketi

ALIGNMENTS

RESULT 1

A56881

prostate-specific membrane antigen - human

C;Species: Homo sapiens (man)

C;Date: 03-Nov-1995 #sequence_revision 03-Nov-1995 #text_change 09-Jul-2004

C;Accession: A56881

R;Israeli, R.S.; Powell, C.T.; Fair, W.R.; Heston, W.D.

Cancer Res. 53, 227-230, 1993

A;Title: Molecular cloning of a complementary DNA encoding a prostate-specific membrane antigen.

A;Reference number: A56881; MUID:93113576; PMID:8417812

A;Accession: A56881

A;Status: preliminary

A;Molecule type: mRNA

A;Residues: 1-750 <ISR>

A;Cross-references: UNIPROT:Q04609; UNIPARC:UPI0000000A01; GB:M99487;

NID:g190663; PIDN:AAA60209.1; PID:g190664

A;Experimental source: prostatic carcinoma cell line LNCaP

A;Note: sequence extracted from NCBI backbone (NCBIN:121724, NCBIP:121725)

C;Superfamily: transferrin receptor

C;Keywords: surface antigen; transmembrane protein

Query Match 34.0%; Score 1307; DB 2; Length 750;
 Best Local Similarity 38.8%; Pred. No. 2.2e-84;
 Matches 293; Conservative 138; Mismatches 267; Indels 58; Gaps 21;

Qy 12 GAAALLG---LGIILGHF-AIPKKANSLAPQDLDLEILETVMGQLDAHRIRENLRSLR 66
 || | | || : | | :| :: |: .: : | | |:: | :|| :

Db 24 GALVLAGGFLLGFLFGWFIKSSNEATNITPK---HNMK AFLDELKAENIKKFLYNFTQ 79

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OM protein - protein search, using sw model

Run on: March 31, 2006, 13:10:09 ; Search time 234 Seconds
(without alignments)
2231.158 Million cell updates/sec

Title: US-09-743-647A-35

Perfect score: 3839

Sequence: 1 MQWTKVLGLGLGAAALLGLG.....SIVVTALEGAAATLRPVADL 740

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2166443 seqs, 705528306 residues

Total number of hits satisfying chosen parameters: 2166443

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : UniProt_05.80:*

1: uniprot_sprot:*

2: uniprot_trembl:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result	No.	Score	Query	%	Match	Length	DB	ID	Description
	1	3838	99.9	740	1	NALDL_HUMAN			Q9uqq1 homo sapien
	2	3135.5	81.7	745	1	NALDL_MOUSE			Q7m758 mus musculu
	3	3124.5	81.4	745	1	NALDL_RAT			Q54697 rattus norv
	4	1840	47.9	1321	2	Q4RSL1_TETNG			Q4rs11 tetraodon n
	5	1321.5	34.4	751	1	FOLH1_PIG			Q77564 s glutamate
	6	1308.5	34.1	738	2	Q5BL58_XENTR			Q5bl58 xenopus tro
	7	1307	34.0	745	2	Q7ZUD9_BRARE			Q7zud9 brachydanio
	8	1307	34.0	750	1	FOLH1_HUMAN			Q04609 h glutamate
	9	1307	34.0	750	2	Q541A4_HUMAN			Q541a4 homo sapien
	10	1299	33.8	740	1	NALD2_HUMAN			Q9y3q0 homo sapien
	11	1299	33.8	740	2	Q4VAM9_HUMAN			Q4vam9 homo sapien
	12	1295.5	33.7	752	1	FOLH1_RAT			P70627 r glutamate
	13	1295.5	33.7	752	2	Q547B6_RAT			Q547b6 rattus norv
	14	1295	33.7	754	2	Q4KLVO_XENLA			Q4klv0 xenopus lae
	15	1278.5	33.3	752	1	FOLH1_MOUSE			O35409 m glutamate
	16	1277.5	33.3	740	1	NALD2_MOUSE			Q9czr2 mus musculu
	17	1200.5	31.3	719	2	Q8TAY3_HUMAN			Q8tay3 homo sapien
	18	990	25.8	770	1	GCP2_CAEBR			Q5wn23 caenorhabdi
	19	976.5	25.4	770	1	GCP2_CAEEL			P91406 caenorhabdi
	20	973.5	25.4	751	2	Q4Z8H5_CAEEL			Q4z8h5 caenorhabdi
	21	942.5	24.6	728	2	Q5JKV3_ORYSA			Q5jkv3 oryza sativ
	22	936	24.4	681	2	Q7Y228_ARATH			Q7y228 arabidopsis
	23	910	23.7	745	2	Q93332_CAEEL			Q93332 caenorhabdi

24	896.5	23.4	774	2	Q610T9_CAEBR	Q610t9 caenorhabd
25	882.5	23.0	705	1	GCP2_ARATH	Q9m1s8 arabidopsis
26	863.5	22.5	442	2	Q9HBA9_HUMAN	Q9hba9 homo sapien
27	814.5	21.2	760	2	Q6CQJ7_KLULA	Q6cqj7 kluyveromyc
28	804	20.9	772	2	Q852M4_ORYSA	Q852m4 oryza sativ
29	790.5	20.6	884	2	Q5B3F5_EMENI	Q5b3f5 aspergillus
30	773	20.1	907	2	Q4WXT7_ASPEFU	Q4wxt7 aspergillus
31	769.5	20.0	790	2	Q7NKV9_GLOVI	Q7nkv9 gloeobacter
32	769	20.0	758	2	Q6CFP0_YARLI	Q6cfp0 yarrowia li
33	766	20.0	925	2	Q7SAE5_NEUCR	Q7sae5 neurospora
34	762	19.8	810	2	Q7SFY6_NEUCR	Q7sfy6 neurospora
35	754	19.6	866	2	Q4PCE6_USTMA	Q4pce6 ustilago ma
36	748.5	19.5	772	2	Q5B612_EMENI	Q5b612 aspergillus
37	742.5	19.3	661	2	Q5JNK6_ORYSA	Q5jnk6 oryza sativ
38	742	19.3	727	2	Q52GB6_MAGGR	Q52gb6 magnaporthe
39	733	19.1	705	2	Q70U68_PHYPO	Q70u68 physarum po
40	731	19.0	942	2	Q560F9_CRYNE	Q560f9 cryptococcu
41	730.5	19.0	745	2	Q51JT1_MAGGR	Q51jt1 magnaporthe
42	727.5	19.0	706	2	Q6J516_PHYPO	Q6j516 physarum po
43	727.5	19.0	724	2	Q4I3R7_GIBZE	Q4i3r7 gibberella
44	722.5	18.8	717	2	Q4II44_GIBZE	Q4ii44 gibberella
45	722.5	18.8	911	2	Q5KPG1_CRYNE	Q5kpg1 cryptococcu

ALIGNMENTS

RESULT 1

NALDL_HUMAN

ID NALDL_HUMAN STANDARD; PRT; 740 AA.
AC Q9UQQ1; O43176;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 13-SEP-2005 (Rel. 48, Last annotation update)
DE **N-acetylated-alpha-linked acidic dipeptidase-like protein**
DE (EC 3.4.17.21) (**NAALADase L**) (Ileal dipeptidylpeptidase) (100 kDa
DE ileum brush border membrane protein) (I100).
GN Name=NAALADL1; Synonyms=NAALADASEL, NAALADL;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC Homo.
OX NCBI_TaxID=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE (ISOFORMS 1; 2; 3; 4; 5; 6; 7 AND 8).
RC TISSUE=Small intestine;
RX MEDLINE=99185063; PubMed=10085079; DOI=10.1074/jbc.274.13.8470;
RA Pangalos M.N., Neefs J.-M., Somers M., Verhasselt P., Bekkers M.,
RA van der Helm L., Fraiponts E., Ashton D., Gordon R.D.;
RT "Isolation and expression of novel human glutamate carboxypeptidases
RT with N-acetylated alpha-linked acidic dipeptidase and dipeptidyl
RT peptidase IV activity.";
RL J. Biol. Chem. 274:8470-8483(1999).
RN [2]
RP NUCLEOTIDE SEQUENCE OF 419-740.
RC TISSUE=Ileum;
RX MEDLINE=98049571; PubMed=9388249; DOI=10.1074/jbc.272.49.31006;
RA Shneider B.L., Thevananther S., Moyer M.S., Walters H.C., Rinaldo P.,
RA Devarajan P., Sun A.Q., Dawson P.A., Ananthanarayanan M.;

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OM protein - protein search, using sw model

Run on: March 31, 2006, 13:09:39 ; Search time 192 Seconds
(without alignments)
1693.439 Million cell updates/sec

Title: US-09-743-647A-35

Perfect score: 3839

Sequence: 1 MQWTKVLGLGLGAAALLGLG.....SIVVTALEGAAATLRPVADL 740

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2443163 seqs, 439378781 residues

Total number of hits satisfying chosen parameters: 2443163

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : A_Geneseq_21:*

1: geneseqp1980s:*

2: geneseqp1990s:*

3: geneseqp2000s:*

4: geneseqp2001s:*

5: geneseqp2002s:*

6: geneseqp2003as:*

7: geneseqp2003bs:*

8: geneseqp2004s:*

9: geneseqp2005s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Query					Description
	Score	Match	Length	DB	ID	
1	3839	100.0	745	4	ABG09829	Abg09829 Novel hum
2	3838	99.9	740	3	AAY58870	Aay58870 Human pep
3	3838	99.9	740	9	ADZ97838	Adz97838 Human NAA
4	3608.5	94.0	705	3	AAY58873	Aay58873 Human pep
5	3603.5	93.9	705	3	AAY58872	Aay58872 Human pep
6	3600.5	93.8	699	3	AAY58871	Aay58871 Human pep
7	3313.5	86.3	687	8	ADI16329	Adi16329 Human pro
8	3226	84.0	635	3	AAY58877	Aay58877 Human pep
9	2947	76.8	578	3	AAY58876	Aay58876 Human pep
10	2637.5	68.7	522	3	AAY58875	Aay58875 Human pep
11	2633.5	68.6	544	3	AAY58874	Aay58874 Human pep
12	1324	34.5	750	3	AAY92640	Aay92640 Mutant hu
13	1309	34.1	750	3	AAB44334	Aab44334 Human PRO
14	1309	34.1	750	4	AAU29075	Aau29075 Human PRO
15	1309	34.1	750	6	ABU58451	Abu58451 Human PRO

16	1309	34.1	750	6	ABU87999	Abu87999 Novel hum
17	1309	34.1	750	6	ABU84314	Abu84314 Human sec
18	1309	34.1	750	6	ABR66188	Abr66188 Human sec
19	1309	34.1	750	6	ABR65578	Abr65578 Human sec
20	1309	34.1	750	6	ABU99518	Abu99518 Human sec
21	1309	34.1	750	6	ABU82757	Abu82757 Human PRO
22	1309	34.1	750	6	ABU89878	Abu89878 Novel hum
23	1309	34.1	750	6	ABR68127	Abr68127 Human sec
24	1309	34.1	750	6	ABU96180	Abu96180 Novel hum
25	1309	34.1	750	6	ABU92611	Abu92611 Human sec
26	1309	34.1	750	6	ABO08688	Abo08688 Human sec
27	1309	34.1	750	6	ABO02740	Abo02740 Human sec
28	1309	34.1	750	6	ABR74894	Abr74894 Human sec
29	1309	34.1	750	6	ABR94656	Abr94656 Human sec
30	1309	34.1	750	6	ABO25280	Abo25280 Novel hum
31	1309	34.1	750	6	ABU85629	Abu85629 Human PRO
32	1309	34.1	750	6	ABU98789	Abu98789 Novel hum
33	1309	34.1	750	6	ABU98004	Abu98004 Novel hum
34	1309	34.1	750	6	ABU91710	Abu91710 Novel hum
35	1309	34.1	750	6	ABU72286	Abu72286 Novel hum
36	1309	34.1	750	6	ABU89403	Abu89403 Human PRO
37	1309	34.1	750	6	ABU86244	Abu86244 Human sec
38	1309	34.1	750	6	ABU67457	Abu67457 Human sec
39	1309	34.1	750	6	ABU80485	Abu80485 Human PRO
40	1309	34.1	750	6	ABR99403	Abr99403 Human sec
41	1309	34.1	750	6	ABR98793	Abr98793 Human sec
42	1309	34.1	750	6	ABO16316	Abo16316 Human sec
43	1309	34.1	750	6	ABR92216	Abr92216 Human sec
44	1309	34.1	750	6	ABO18857	Abo18857 Human sec
45	1309	34.1	750	6	ABR78278	Abr78278 Human sec

ALIGNMENTS

RESULT 1

ABG09829

ID ABG09829 standard; protein; 745 AA.
 AC ABG09829;
 DT 13-FEB-2002 (first entry)
 DE Novel human diagnostic protein #9820.
 KW Human; chromosome mapping; gene mapping; gene therapy; forensic;
 KW food supplement; medical imaging; diagnostic; genetic disorder.
 OS Homo sapiens.
 PN WO200175067-A2.
 PD 11-OCT-2001.
 PF 30-MAR-2001; 2001WO-US008631.
 PR 31-MAR-2000; 2000US-00540217.
 PR 23-AUG-2000; 2000US-00649167.
 PA (HYSE-) HYSEQ INC.
 PI Drmanac RT, Liu C, Tang YT;
 DR WPI; 2001-639362/73.
 DR N-PSDB; AAS74016.
 PT New isolated polynucleotide and encoded polypeptides, useful in
 PT diagnostics, forensics, gene mapping, identification of mutations
 PT responsible for genetic disorders or other traits and to assess
 PT biodiversity.
 PS Claim 20; SEQ ID NO 40188; 103pp; English.

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OM protein - nucleic search, using frame_plus_p2n model
Run on: March 31, 2006, 17:07:00 ; Search time 345 Seconds
(without alignments)
3812.741 Million cell updates/sec

Title: US-09-743-647A-35
Perfect score: 3839
Sequence: 1 MQWTKVLGLGLGAAALLGLG.....SIVVTALEGAATLRPVADL 740

Scoring table: BLOSUM62
Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 1303057 seqs, 888780828 residues
Total number of hits satisfying chosen parameters: 2606114
Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Command line parameters:

```
-MODEL=frame+_p2n.model -DEV=xlh
-Q=/abss/ABSSWEB_spool/US09743647/runat_31032006_094835_15847/app_query.fasta_1
-DB=Issued_Patents_NA -QFMT=fastap -SUFFIX=p2n.rni -MINMATCH=0.1 -LOOPCL=0
-LOOPEXT=0 -UNITS=bits -START=1 -END=-1 -MATRIX=blosum62 -TRANS=human40.cdi
-LIST=45 -DOCALIGN=200 -THR_SCORE=pct -THR_MAX=100 -THR_MIN=0 -ALIGN=15
-MODE=LOCAL -OUTFMT=pto -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000
-HOST=abss07 -USER=US09743647@CGN_1_1_193@runat_31032006_094835_15847
-NCPU=6 -ICPU=3 -NO_MMAP -NEG_SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG
-DEV_TIMEOUT=120 -WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7
```

Database : Issued_Patents_NA:
1: /cgn2_6/ptodata/1/ina/1_COMB.seq:*
2: /cgn2_6/ptodata/1/ina/5_COMB.seq:*
3: /cgn2_6/ptodata/1/ina/6A_COMB.seq:*
4: /cgn2_6/ptodata/1/ina/6B_COMB.seq:*
5: /cgn2_6/ptodata/1/ina/H_COMB.seq:*
6: /cgn2_6/ptodata/1/ina/PCTUS_COMB.seq:*
7: /cgn2_6/ptodata/1/ina/PP_COMB.seq:*
8: /cgn2_6/ptodata/1/ina/RE_COMB.seq:*
9: /cgn2_6/ptodata/1/ina/backfiles1.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result	Query					Description
	No.	Score	Match	Length	DB	
<hr/>						
1	1309	34.1	2558	3	US-09-999-833A-617	Sequence 617, App

2	1309	34.1	2558	3	US-10-020-445A-617	Sequence 617, App	
3	1307	34.0	2653	2	US-08-325-553-1	Sequence 1, Appli	
4	1307	34.0	2653	2	US-08-394-152A-1	Sequence 1, Appli	
5	1307	34.0	2653	3	US-08-705-477E-1	Sequence 1, Appli	
6	1307	34.0	2653	3	US-09-973-382C-3	Sequence 3, Appli	
7	1307	34.0	2653	3	US-08-466-381C-1	Sequence 1, Appli	
8	1293.5	33.7	2133	3	US-09-164-034B-1	GENERAL INFORMATION	
9	1282.5	33.4	2387	3	US-08-705-477E-100	Sequence 100, App	
10	1040	27.1	1992	3	US-09-973-382C-1	Sequence 1, Appli	
11	709	18.5	2877	3	US-09-358-755-2	Sequence 2, Appli	
12	705	18.4	2519	3	US-09-358-755-3	Sequence 3, Appli	
13	645.5	16.8	2513	3	US-09-949-016-1366	Sequence 1366, Ap	
14	593.5	15.5	2826	3	US-09-023-655-1324	Sequence 1324, Ap	
15	593.5	15.5	4080	3	US-09-016-434-1352	Sequence 1352, Ap	
16	593.5	15.5	5010	3	US-09-161-244-1	Sequence 1, Appli	
17	578.5	15.1	8731	3	US-09-919-039-350	Sequence 350, App	
18	391.5	10.2	915	3	US-09-248-796A-6742	Sequence 6742, Ap	
19	318	8.3	780	2	US-08-325-553-27	Sequence 27, Appli	
20	318	8.3	780	2	US-08-394-152A-27	Sequence 27, Appli	
21	318	8.3	780	3	US-08-705-477E-27	Sequence 27, Appli	
22	318	8.3	780	3	US-08-466-381C-27	Sequence 27, Appli	
23	305	7.9	2352	3	US-09-614-221A-77	Sequence 77, Appli	
24	284	7.4	1185	3	US-09-248-796A-6116	Sequence 6116, Ap	
25	274	7.1	624	3	US-09-533-559-747	Sequence 747, App	
26	265	6.9	540	2	US-08-325-553-29	Sequence 29, Appli	
27	265	6.9	540	2	US-08-394-152A-29	Sequence 29, Appli	
28	265	6.9	540	3	US-08-705-477E-29	Sequence 29, Appli	
29	265	6.9	540	3	US-08-466-381C-29	Sequence 29, Appli	
30	226	5.9	660	2	US-08-325-553-28	Sequence 28, Appli	
31	226	5.9	660	2	US-08-394-152A-28	Sequence 28, Appli	
32	226	5.9	660	3	US-08-705-477E-28	Sequence 28, Appli	
33	226	5.9	660	3	US-08-466-381C-28	Sequence 28, Appli	
c	34	222.5	5.8	11358	3	US-09-902-540-1075	Sequence 1075, Ap
	35	220.5	5.7	1317	3	US-09-902-540-9439	Sequence 9439, Ap
	36	220.5	5.7	1584	3	US-09-248-796A-6743	Sequence 6743, Ap
c	37	216.5	5.6	231	3	US-09-439-313-454	Sequence 454, App
c	38	216.5	5.6	231	3	US-09-352-616A-454	Sequence 454, App
c	39	216.5	5.6	231	3	US-09-636-215-454	Sequence 454, App
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c	41	216.5	5.6	231	3	US-09-679-426-454	Sequence 454, App
c	42	216.5	5.6	231	3	US-09-759-143-454	Sequence 454, App
c	43	216.5	5.6	231	3	US-09-651-236-454	Sequence 454, App
c	44	216.5	5.6	231	3	US-09-657-279-454	Sequence 454, App
c	45	216.5	5.6	231	3	US-10-012-896-454	Sequence 454, App

ALIGNMENTS

RESULT 1

US-09-999-833A-617

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; Sequence 617, Application US/09999833A
; Patent No. 6916648
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi
; APPLICANT: Baker Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan
; APPLICANT: Ferrara, Napoleon
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GenCore version 5.1.7
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OM protein - protein search, using sw model
Run on: March 31, 2006, 13:28:40 ; Search time 167 Seconds
(without alignments)
1851.459 Million cell updates/sec

Title: US-09-743-647A-35
Perfect score: 3839
Sequence: 1 MQWTKVLGLGLGAAALLGLG.....SIVVTALEGAAATLRPVADL 740

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5
Searched: 1867569 seqs, 417829326 residues
Total number of hits satisfying chosen parameters: 1867569
Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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2: /cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB.pep:*

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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		Match	Length	DB	ID	
1	3839	100.0	745	5	US-10-450-763-40188	Sequence 40188, A
2	1309	34.1	750	3	US-09-978-295A-618	Sequence 618, App
3	1309	34.1	750	3	US-09-978-697-618	Sequence 618, App
4	1309	34.1	750	3	US-09-978-192A-618	Sequence 618, App
5	1309	34.1	750	3	US-09-999-832A-618	Sequence 618, App
6	1309	34.1	750	3	US-09-978-189-618	Sequence 618, App
7	1309	34.1	750	3	US-09-978-608A-618	Sequence 618, App
8	1309	34.1	750	3	US-09-978-585A-618	Sequence 618, App
9	1309	34.1	750	3	US-09-978-191A-618	Sequence 618, App
10	1309	34.1	750	3	US-09-978-403A-618	Sequence 618, App
11	1309	34.1	750	3	US-09-978-564A-618	Sequence 618, App
12	1309	34.1	750	3	US-09-999-833A-618	Sequence 618, App
13	1309	34.1	750	3	US-09-981-915A-618	Sequence 618, App
14	1309	34.1	750	3	US-09-978-824-618	Sequence 618, App
15	1309	34.1	750	3	US-09-918-585A-618	Sequence 618, App
16	1309	34.1	750	3	US-09-999-834A-618	Sequence 618, App
17	1309	34.1	750	3	US-09-978-423A-618	Sequence 618, App
18	1309	34.1	750	3	US-09-978-193A-618	Sequence 618, App
19	1309	34.1	750	3	US-09-999-830A-618	Sequence 618, App

20	1309	34.1	750	3	US-09-978-757A-618	Sequence 618, App
21	1309	34.1	750	3	US-09-978-187B-618	Sequence 618, App
22	1309	34.1	750	3	US-09-978-643A-618	Sequence 618, App
23	1309	34.1	750	3	US-09-978-375A-618	Sequence 618, App
24	1309	34.1	750	3	US-09-978-298A-618	Sequence 618, App
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26	1309	34.1	750	3	US-09-978-681A-618	Sequence 618, App
27	1309	34.1	750	3	US-09-978-194A-618	Sequence 618, App
28	1309	34.1	750	3	US-09-999-829A-618	Sequence 618, App
29	1309	34.1	750	3	US-09-978-299A-618	Sequence 618, App
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32	1309	34.1	750	3	US-09-978-802A-618	Sequence 618, App
33	1309	34.1	750	3	US-09-999-831A-618	Sequence 618, App
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36	1309	34.1	750	4	US-10-174-590-104	Sequence 104, App
37	1309	34.1	750	4	US-10-176-758-104	Sequence 104, App
38	1309	34.1	750	4	US-10-175-737-104	Sequence 104, App
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43	1309	34.1	750	4	US-10-176-915-104	Sequence 104, App
44	1309	34.1	750	4	US-10-173-706-104	Sequence 104, App
45	1309	34.1	750	4	US-10-175-738-104	Sequence 104, App

ALIGNMENTS

RESULT 1

US-10-450-763-40188

; Sequence 40188, Application US/10450763
; Publication No. **US20050196754A1**

; GENERAL INFORMATION:

; APPLICANT: Hyseq, Inc
; TITLE OF INVENTION: NOVEL NUCLEIC ACIDS AND POLYPEPTIDES
; FILE REFERENCE: 790CIP3/US
; CURRENT APPLICATION NUMBER: **US/10/450,763**
; CURRENT FILING DATE: **2003-06-11**
; PRIOR APPLICATION NUMBER: **PCT/US01/08631**
; PRIOR FILING DATE: **2001-03-30**
; PRIOR APPLICATION NUMBER: **09/540,217**
; PRIOR FILING DATE: **2000-03-31**
; PRIOR APPLICATION NUMBER: **09/649,167**
; PRIOR FILING DATE: **2000-08-23**
; NUMBER OF SEQ ID NOS: 60736
; SOFTWARE: Custom
; SEQ ID NO 40188
; LENGTH: 745
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE: DOMAIN LOCATION: (167)..(259)
; OTHER INFORMATION: PA domain identified by PFam, accession name PA, E-value=5.8e
; OTHER INFORMATION: -21, PFam score of 83.1

US-10-450-763-40188

Query Match **100.0%**; Score 3839; DB 5; Length 745;
Best Local Similarity **99.9%**; Pred. No. 0;
Matches 739; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

GenCore version 5.1.7
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OM protein - protein search, using sw model

Run on: March 31, 2006, 13:29:45 ; Search time 26 Seconds
(without alignments)
866.423 Million cell updates/sec

Title: US-09-743-647A-35

Perfect score: 3839

Sequence: 1 MQWTKVLGLGLGAAALLGLG.....SIVVTALEGAATLRPVADL 740

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 180808 seqs, 30441898 residues

Total number of hits satisfying chosen parameters: 180808

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published_Applications_AA_New:*

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- 2: /SIDS5/ptodata/2/pubpaa/US06_NEW_PUB.pep:*
- 3: /SIDS5/ptodata/2/pubpaa/US07_NEW_PUB.pep:*
- 4: /SIDS5/ptodata/2/pubpaa/PCT_NEW_PUB.pep:*
- 5: /SIDS5/ptodata/2/pubpaa/US09_NEW_PUB.pep:*
- 6: /SIDS5/ptodata/2/pubpaa/US10_NEW_PUB.pep:*
- 7: /SIDS5/ptodata/2/pubpaa/US11_NEW_PUB.pep:*
- 8: /SIDS5/ptodata/2/pubpaa/US60_NEW_PUB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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1	1307	34.0	750	7	US-11-073-347-1 Sequence 1, Appli
2	1307	34.0	750	7	US-11-155-288-4 Sequence 4, Appli
3	1307	34.0	750	7	US-11-202-516-2 Sequence 2, Appli
4	1294.5	33.7	752	7	US-11-202-516-8 Sequence 8, Appli
5	1276.5	33.3	694	7	US-11-202-516-10 Sequence 10, Appli
6	709	18.5	801	6	US-10-453-372-466 Sequence 466, App
7	705	18.4	801	6	US-10-453-372-468 Sequence 468, App
8	583.5	15.2	760	6	US-10-912-580-4 Sequence 4, Appli
9	583.5	15.2	760	6	US-10-912-585-1 Sequence 1, Appli
10	561.5	14.6	804	6	US-10-912-580-5 Sequence 5, Appli
11	561.5	14.6	804	6	US-10-912-585-2 Sequence 2, Appli
12	391	10.2	489	6	US-10-453-372-460 Sequence 460, App
13	248.5	6.5	424	6	US-10-453-372-458 Sequence 458, App
14	135.5	3.5	1171	6	US-10-467-657-7842 Sequence 7842, Ap
15	116.5	3.0	909	7	US-11-077-619-8 Sequence 8, Appli
16	114.5	3.0	1140	6	US-10-858-730-208 Sequence 208, App
17	113.5	3.0	2523	7	US-11-052-554A-143 Sequence 143, App

18	108	2.8	2399	7	US-11-052-554A-92	Sequence 92, Appl
19	107.5	2.8	462	7	US-11-087-099-3504	Sequence 3504, Ap
20	107.5	2.8	462	7	US-11-087-099-11772	Sequence 11772, A
21	106.5	2.8	565	7	US-11-096-568A-1994	Sequence 1994, Ap
22	106.5	2.8	565	7	US-11-096-568A-27236	Sequence 27236, A
23	106.5	2.8	624	7	US-11-096-568A-1993	Sequence 1993, Ap
24	106.5	2.8	624	7	US-11-096-568A-27235	Sequence 27235, A
25	106.5	2.8	625	7	US-11-096-568A-1992	Sequence 1992, Ap
26	106.5	2.8	625	7	US-11-096-568A-27234	Sequence 27234, A
27	106	2.8	943	6	US-10-467-657-5508	Sequence 5508, Ap
28	104.5	2.7	797	7	US-11-090-617-554	Sequence 554, App
29	103.5	2.7	791	6	US-10-821-234-962	Sequence 962, App
30	103	2.7	1158	6	US-10-858-730-70	Sequence 70, Appl
31	102.5	2.7	878	6	US-10-954-468-41	Sequence 41, Appl
32	101	2.6	1234	6	US-10-995-561-870	Sequence 870, App
33	101	2.6	1365	6	US-10-995-561-867	Sequence 867, App
34	101	2.6	1366	6	US-10-995-561-868	Sequence 868, App
35	101	2.6	1411	6	US-10-995-561-869	Sequence 869, App
36	99.5	2.6	1047	7	US-11-067-260-16	Sequence 16, Appl
37	99.5	2.6	1082	7	US-11-067-260-15	Sequence 15, Appl
38	99.5	2.6	1263	7	US-11-076-163-3	Sequence 3, Appl
39	99.5	2.6	1312	7	US-11-067-260-20	Sequence 20, Appl
40	99.5	2.6	1312	7	US-11-067-260-32	Sequence 32, Appl
41	99.5	2.6	1389	7	US-11-067-260-52	Sequence 52, Appl
42	99.5	2.6	1392	7	US-11-067-260-24	Sequence 24, Appl
43	99.5	2.6	1403	7	US-11-067-260-58	Sequence 58, Appl
44	99.5	2.6	1444	7	US-11-067-260-46	Sequence 46, Appl
45	99.5	2.6	1447	7	US-11-067-260-22	Sequence 22, Appl

ALIGNMENTS

RESULT 1

US-11-073-347-1

; Sequence 1, Application US/11073347
; Publication No. US20050260234A1
; GENERAL INFORMATION:
; APPLICANT: SIMARD, John J. L.
; APPLICANT: DIAMOND, David C.
; TITLE OF INVENTION: ANTI-NEOVASCULATURE PREPARATIONS FOR CANCER
; FILE REFERENCE: MANNK.015C1
; CURRENT APPLICATION NUMBER: US/11/073,347
; CURRENT FILING DATE: 2005-03-04
; PRIOR APPLICATION NUMBER: 10/094,699
; PRIOR FILING DATE: 2002-03-07
; PRIOR APPLICATION NUMBER: 60/274,063
; PRIOR FILING DATE: 2001-03-07
; NUMBER OF SEQ ID NOS: 159
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 750
; TYPE: PRT
; ORGANISM: Homo sapien

US-11-073-347-1

Query Match 34.0%; Score 1307; DB 7; Length 750;
Best Local Similarity 38.8%; Pred. No. 7.3e-102;
Matches 293; Conservative 138; Mismatches 267; Indels 58; Gaps 21;